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<110> RIKEN

<120> Truncated Reelin Protein and DNA Encoding the Same

<130> PH-1167

<140>

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<150> JP 2000-109954

<151> 2000-04-11

<160> 28

<170> PatentIn Ver. 2.0

<210> 1

<211> 2274

<212> DNA

<213> Xenopus laevis

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<221> CDS

<222> (157)..(1455)

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<222> (241)..(726)

<223> F-spondin domain

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<222> (847)..(1197)

<223> CR-50 epitope region

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atgaagaaag ctcatthaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174

Met Glu Leu Leu His Thr

1

5

ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222

Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys

10

15

20

ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270

Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe

25

30

35

ttt ttc ctt tgc act cat cat gga gaa ctg gaa gga gat ggg gaa caa 318  
Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu Gln

40

45

50

gga gaa gtg ctc atc tct ctg cac ctg gcg ggc aac ccc agc tac tac 366  
Gly Glu Val Leu Ile Ser Leu His Leu Ala Gly Asn Pro Ser Tyr Tyr

55

60

65

70

ata cct ggg cag gag tac cat gtg acc ata tcc act agt acc ttc ttt 414  
Ile Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe Phe

75

80

85

gat ggt ctt ctg gtg act gga ctt tac act tct acc agt gtt caa gcg 462  
Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Val Gln Ala

90

95

100

tct cag agc att gga ggc tct aaa gca ttt gga ttt ggt att atg agc 510  
Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe Gly Phe Gly Ile Met Ser

105

110

115

gac cgt cag ttt ggt acc cag ttt atg tgc agt gtc gtt gct tcc cac 558  
Asp Arg Gln Phe Gly Thr Gln Phe Met Cys Ser Val Val Ala Ser His

120

125

130

gtg agt cat ctt ccc aca aca aac cta agt ttt gta tgg att gca cca 606  
Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe Val Trp Ile Ala Pro

135

140

145

150

cca gca ggt aca gga tgt gtc aac ttc atg gcc aca gca aca cat agg 654

Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His Arg

155

160

165

gga caa gtt att ttc aag gat gcc ctg gca caa caa ctg tgc gaa caa 702

Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu Gln

170

175

180

gga gct cct act gaa gct ccc ttg cgg cct aat tta gcc gaa att cac 750

Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro Asn Leu Ala Glu Ile His

185

190

195

agt gaa agc atc ctt tta cga gat gat ttt gac tca tat aag ctt cag 798

Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe Asp Ser Tyr Lys Leu Gln

200

205

210

gaa ttg aat cca aat att tgg ctc cag tgc aga aat tgc gaa gtt ggt 846

Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys Arg Asn Cys Glu Val Gly

215

220

225

230

gag cag tgt ggt gca att atg cat ggt ggg gca gtc act ttt tgt gat 894

Glu Gln Cys Gly Ala Ile Met His Gly Gly Ala Val Thr Phe Cys Asp

235

240

245

ccg tat gga cca aga gaa ttg ata act gtt caa atg aac aca act acg 942

Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val Gln Met Asn Thr Thr Thr

250

255

260

gca tct gtt ttg cag ttt tct att ggg tca gga tcg tgc agg ttc agc 990

Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe Ser

275

Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr Thr Lys Asn Asn Ser Ser

290

Ser Trp Met Pro Leu Glu Arg Ile Ser Ala Pro Ser Asn Val Ser Thr

310

Ile Ile His Ile Ile Tyr Leu Pro Pro Glu Ala Lys Gly Glu Asn Val

325

Lys Phe Arg Trp Arg Gln Glu Asn Met Gln Ala Gly Asp Val Tyr Glu

340

Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile Ile Asn Ala Ala His Lys

355

Glu Val Val Leu Glu Asp Asn Leu Asp Pro Met Asp Thr Gly Asn Trp

370

Leu Phe Phe Pro Gly Ala Thr Val Lys His Thr Cys Gln Ser Asp Gl

390



tcttgtacct tgcatacat ttgtggctag tttatgggtc aatagacagc catcatacat 2015

tagtcagagt aaatcgagca ttacaaaact caatgagcca tagtgagtgt gacaatcaga 2075

agtgactgtc aagtaaatca accatttgct catacagatg cacatttgaa cagtggattc 2135

ttatccagaa agggccattt ttactatca ctctgggatt taaatgccac ttctaattgg 2195

aacttccagg tcacaaaaat agaatggaca tttaaaccatc atggttctca ttaccacctaa 2255

taaaactccg gttttttta 2274

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<212> PRT

<213> *Xenopus laevis*

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1

5

10

15

Phe Thr Gly Ile Leu Cys Phe Val Val Ala Arg Gly Val Gly Tyr Tyr

20

25

30

Pro Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu

35

40

45

Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala

50

55

60

Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile

65

70

75

80

Ser Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr

85

90

95

Ser Thr Ser Val Gln Ala Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe

100

105

110

Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys

115

120

125

Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser

130

135

140

Phe Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met

145

150

155

160

Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala

165

170

175

Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro

180

185

190

Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe

195

200

205



Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys  
210 215 220

Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly  
225 230 235 240

Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val  
245 250 255

Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser  
260 265 270

Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr  
275 280 285

Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala  
290 295 300

Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu  
305 310 315 320

Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln  
325 330 335

Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile  
340 345 350

Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro  
355 360 365

Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His

370

375

380

Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser

385

390

395

400

Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu

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410

415

Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly

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<210> 3

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<213> Mus musculus

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<222> (283)..(2052)

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<222> (284)..(849)

<223> F-spondin domain

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tcggtctccc gctaacttcc ccccgcgggc tcggttgccc ggaccgcgc ggctcgagcc 180

cgccgcccggc tcgccttccc cgcacgcggc tcctccgtgc cggcgcctcc gaaagtggat 240

gagagagcgc gcggggcgcg cggcggcacg gagcgcggcg gc atg gag cgc ggc 294

Met Glu Arg Gly

1

tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg gcg 342

Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala

5

10

15

20

acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390

Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro

25

30

35





265

270

275

agt tac tct gac ccc agc atc act gtg tca tac gcc aag aac aat acc 1158  
 Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr

280

285

290

gct gat tgg att cag ctg gag aaa att aga gcc cct tcc aat gtg agc 1206  
 Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser  
 295 300 305

aca gtc atc cac atc ctg tac ctc ccc gag gaa gcc aaa ggg gag agc 1254  
 Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser  
 310 315 320

gtg cag ttc cag tgg aaa cag gac agc ctg cga gtg ggt gag gtg tat 1302  
 Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr  
 325 330 335 340

gag gcc tgc tgg gcc ctg gat aac atc ctg gtc atc aat tca gcc cac 1350  
 Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile Asn Ser Ala His  
 345 350 355

aga gaa gtc gtt ctg gag gac aac ctc gac ccg gtc gac acg ggc aac 1398  
 Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val Asp Thr Gly Asn  
 360 365 370

tgg ctc ttc ttc cct gga gca acg gtc aag cat agc tgt cag tca gat 1446  
 Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser Cys Gln Ser Asp  
 375 380 385

ggg aac tcc att tat ttc cat gga aat gaa ggc agc gag ttc aat ttt 1494  
Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser Glu Phe Asn Phe

390

395

400

gcc acc acc cgg gat gta gat ctt tct aca gag gat att caa gag cag 1542  
Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp Ile Gln Glu Gln

405

410

415

420

tgg tca gaa gaa ttt gag agc cag ccc aca gga tgg gat atc ttg gga 1590  
Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp Asp Ile Leu Gly

425

430

435

gca gta gtt ggt gca gac tgt gga acc gta gaa tca gga cta tca ctg 1638  
Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser Gly Leu Ser Leu

440

445

450

gtg ttc ctc aaa gat gga gag agg aag ctt tgc acc ccc tac atg gat 1686  
Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr Pro Tyr Met Asp

455

460

465

aca act ggt tat ggc aac ctg agg ttc tac ttc gtt atg gga gga atc 1734  
Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val Met Gly Gly Ile

470

475

480

tgt gac cct gga gtc tct cat gaa aac gat atc atc tta tat gca aag 1782  
Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile Leu Tyr Ala Lys

485

490

495

500

att gaa gga aga aaa gaa cac att gca ctg gac act ctt acc tat tct 1830

Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr Leu Thr Tyr Ser

505

510

515

tcc tat aag gtt ccg tct ttg gtt tct gtg gtc atc aac cct gaa ctt 1878

Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile Asn Pro Glu Leu

520

525

530

cag aca cct gcc acc aaa ttt tgt ctc agg caa aag agc cac caa ggg 1926

Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys Ser His Gln Gly

535

540

545

tat aat cgg aat gtc tgg gct gtg gac ttc ttc cat gtg ctg ccc gtt 1974

Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His Val Leu Pro Val

550

555

560

ctc cct tca aca atg tct cac atg atc cag ttt tct att aat ttg gga 2022

Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser Ile Asn Leu Gly

565

570

575

580

tgc ggc aca cac cag cct ggg aac agg tga gaagcatgcc gagtgccta 2072

Cys Gly Thr His Gln Pro Gly Asn Arg

585

590

acatggtagg aaataaacac atgcactgga ccattgaagt aagtttgtca gtaggatttt 2132

tggatgggat tttaacaaaa tatccattaa gaaaatacag attcctactc cctccctaaa 2192

agagttcttt ggtaataaaa tagaagggat gtgactgggt agatttttag gttagaatag 2252



tttcattcag ggagcttgat acaagttatc agaggtgttc accatgctgt gtggcagcat 2312

ccccgttct aacagattgc tgggtgaaga tgactgaaga caagattggc ttctgttggc 2372

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gctcctcttg cataagtgtt gctcccatcc tctgtaaaga actttgctga cctcacattc 2492

acaggatgaa gtgacagtgt gagacatggt aattgcctag ctatctatca aattcaagag 2552

cacaaacca gtttactgtg tattgtcctt cagacgtagc ttttatggca gtaatccaat 2612

ggcttgccct ctgaaggctg gtcaggcttc agtgagagat gacacattta gtaaaggctc 2672

tagagaaatc ccacattcat cgactcattc aaggatttta gctagaaata aaaagaatca 2732

aaaaaataaa tta 2745

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<211> 589

<212> PRT

<213> Mus musculus

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Leu Leu Leu Ala Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro

20

25

30

Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu

35

40

45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly

50

55

60

Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser

65

70

75

80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser

85

90

95

Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly

100

105

110

Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser

115

120

125

Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe

130

135

140

Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala

145

150

155

160

Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln

165

170

175

Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His  
180 185 190

Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp  
195 200 205

Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser  
210 215 220

Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala  
225 230 235 240

Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys  
245 250 255

Leu Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly  
260 265 270

Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala  
275 280 285

Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro  
290 295 300

Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala  
305 310 315 320

Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val

335

350

365

380

400

415

430

445

460

480

Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile

485

490

495

Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr

500

505

510

Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile

515

520

525

Asn Pro Glu Leu Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys

530

535

540

Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His

545

550

555

560

Val Leu Pro Val Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser

565

570

575

Ile Asn Leu Gly Cys Gly Thr His Gln Pro Gly Asn Arg

580

585

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA



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<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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cagcaacaca taggggacaa

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<210> 9

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

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ggccacgcgt cgactagtac gaattcatct atagcttttt tttttttttt t

51

<210> 10  
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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

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cgacaggtac aggatgtgtc aacttcattg ccaca

35

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 12

tcccacaaca aacctaagtt

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<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 13

atgtcctcac tggaaagatc

20

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 14

cgggataaca ttcagggtat cact

24

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

**Q**uestions may arise as to whether the results are due to the fact that the study was conducted in a hospital setting or if there were other factors involved.

[illegible][illegible][illegible][illegible][illegible][illegible]

**Q**uestions may arise as to whether the results are due to the fact that the subjects were all male or if there was some other factor involved.

[illegible][illegible][illegible][illegible]

1. The first step is to identify the problem. This involves understanding the current situation and the goals that need to be achieved.

<223> Description of Artificial Sequence:synthetic DNA

aggtagcaca tggacaaaat cc

22

**<211> 26**

### <213> Artificial Sequence

**<223> Description of Artificial Sequence: synthetic DNA**

ctgaagcaaa ccagtcaccg tgggtca

26

&lt;211&gt; 25

### <213> Artificial Sequence

<223> Description of Artificial Sequence:synthetic DNA

[illegible]

7

<210> 20

**<211> 21**

## <212> DNA

### <213> Artificial Sequence

**<220>**

<223> Description of Artificial Sequence:synthetic DNA

**<400> 20**

ggccctttct ggataagaat c

21

**<210> 21**

&lt;211&gt; 27

## <212> DNA

### <213> Artificial Sequence

**<220>**

<223> Description of Artificial Sequence:synthetic DNA

**<400> 21**

tcaaccattt gctcatcacg atgcaca

27

&lt;210&gt; 22



<223> Description of Artificial Sequence:synthetic DNA

<400> 24

gcggacaaca atatgcaagg

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<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

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ggttggtgac aaactggtcc

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<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

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cgcgctcgact agtacgaatt

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 27

ctgattggat tcagctggag

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<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 28

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